AMENDMENTS TO THE CLAIMS

1. - 35. (canceled)

36. (currently amended) A method of determining whether a human has an increased risk for developing RF-positive rheumatoid arthritis, comprising testing nucleic acid from said human for the presence or absence of at least one T allele at a polymorphism in gene *PTPN22* ~~a single nucleotide polymorphism (SNP)~~ at position 101 of SEQ ID NO: 36673 or at least one A allele at position 101 of its complement, wherein the presence of said ~~at least one~~ T allele ~~at the SNP based on the sequence orientation of SEQ ID NO:36673~~ or said ~~at least one~~ A allele ~~at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673~~ indicates said human has an increased risk for developing said RF-positive rheumatoid arthritis.

37-40. (canceled)

41. (previously presented) The method of claim 36, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human.

42. (previously presented) The method of claim 41 in which said biological sample is blood, saliva, or buccal cells.

43. (previously presented) The method of claim 36, wherein said testing comprises nucleic acid amplification.

44. (currently amended) The method of claim 36, wherein said testing is performed using at least one detection reagent selected from the group consisting of detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

45. (previously presented) The method of claim 36, wherein said testing is performed using sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size

analysis, single-stranded conformation polymorphism, or denaturing gradient gel electrophoresis (DGGE).

46. (currently amended) A method of determining whether a human has a decreased risk for developing RF-positive rheumatoid arthritis, comprising testing nucleic acid from said human for the presence or absence of a homozygous C/C genotype at a polymorphism in gene *PTPN22* ~~single nucleotide polymorphism (SNP)~~ at position 101 of SEQ ID NO: 36673 or a homozygous G/G genotype at position 101 of its complement, wherein the presence of said [[a]] homozygous C/C genotype ~~at the SNP based on the sequence orientation of SEQ ID NO:36673~~ or said [[a]] homozygous G/G genotype ~~at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673~~ indicates said human has a decreased risk for developing said RF-positive rheumatoid arthritis.

47-50. (canceled)

51. (previously presented) The method of claim 46, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human.

52. (previously presented) The method of claim 51 in which said biological sample is blood, saliva, or buccal cells.

53. (previously presented) The method of claim 46, wherein said testing comprises nucleic acid amplification.

54. (currently amended) The method of claim 46, wherein said testing is performed using at least one detection reagent selected from the group consisting of detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

55. (previously presented) The method of claim 46, wherein said testing is performed using sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size

analysis, single-stranded conformation polymorphism, or denaturing gradient gel electrophoresis (DGGE).

56. (currently amended) A method of determining a human's risk for developing RF-positive rheumatoid arthritis, comprising testing nucleic acid from said human for the presence or absence of a T allele or a C allele at a polymorphism in gene *PTPN22* ~~a single nucleotide polymorphism (SNP)~~ at position 101 of SEQ ID NO: 36673 or an A allele or a G allele at position 101 of its complement, wherein the presence of at least one of said T allele ~~at the SNP based on the sequence orientation of SEQ ID NO:36673~~ or at least one of said A allele ~~at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673~~ indicates said human has an increased risk for developing said RF-positive rheumatoid arthritis, or the presence of two of said C alleles (a homozygous C/C genotype) or two of said G alleles (a homozygous G/G genotype) ~~a homozygous C/C genotype at the SNP based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673~~ indicates said human has a decreased risk for developing said RF-positive rheumatoid arthritis.

57-60. (canceled)

61. (previously presented) The method of claim 56, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human.

62. (previously presented) The method of claim 61 in which said biological sample is blood, saliva, or buccal cells.

63. (previously presented) The method of claim 56, wherein said testing comprises nucleic acid amplification.

64. (currently amended) The method of claim 56, wherein said testing is performed using at least one detection reagent selected from the group consisting of detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

65. (previously presented) The method of claim 56, wherein said testing is performed using sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, single-stranded conformation polymorphism, or denaturing gradient gel electrophoresis (DGGE).

66. (currently amended) The method of any one of claims 36, 46, and 56, further comprising providing a report of the identity of said polymorphism ~~SNP~~.

67. (previously presented) The method of any one of claims 36, 46, and 56, further comprising providing a report of said human's risk for developing RF-positive rheumatoid arthritis.

68. (previously presented) The method of claim 67, wherein the risk is an increased risk for developing RF-positive rheumatoid arthritis.

69. (previously presented) The method of claim 67, wherein the risk is a decreased risk for developing RF-positive rheumatoid arthritis.

70. (currently amended) The method of claim 67, wherein the report further shows the identity of said polymorphism ~~SNP~~.

71. (currently amended) The method of claim 70, wherein the identity of said polymorphism ~~SNP~~ is said ~~at least one~~ T allele ~~based on the sequence orientation of SEQ ID NO:36673~~ or said ~~at least one~~ A allele ~~based on the sequence orientation of the complement of SEQ ID NO:36673~~, and wherein the report indicates said human has an increased risk for developing RF-positive rheumatoid arthritis.

72. (currently amended) The method of claim 70, wherein the identity of said polymorphism ~~SNP~~ is said [[a]] homozygous C/C genotype ~~based on the sequence orientation of SEQ ID NO:36673~~ or said [[a]] homozygous G/G genotype ~~based on the sequence orientation of the complement of SEQ ID NO:36673~~, and wherein the report indicates said human has a decreased risk for developing RF-positive rheumatoid arthritis.

73. (previously presented) The method of claim 66, wherein the report is in paper form or computer readable medium form.

74. (currently amended) The method of claim 36 ~~any one of claims 36, 46, and 56~~, wherein said testing is performed using an allele-specific method.

75. (previously presented) The method of claim 74, wherein said allele-specific method is allele-specific probe hybridization, allele-specific primer extension, or allele-specific amplification.

76. (previously presented) The method of claim 74, wherein said allele-specific method detects said T allele or said A allele.

77. (previously presented) The method of any one of claims 41, 51, and 61, further comprising preparing said nucleic acid extract from said biological sample prior to said testing.

78. (previously presented) The method of claim 77, further comprising obtaining said biological sample from said human prior to said preparing.

79. (previously presented) The method of any one of claims 43, 53, and 63, wherein said nucleic acid amplification is carried out by polymerase chain reaction.

80. (previously presented) The method of claim 36, further comprising correlating the presence of said T allele or said A allele with an increased risk for RF-positive rheumatoid arthritis.

81. (previously presented) The method of claim 46, further comprising correlating the presence of said homozygous C/C genotype or said homozygous G/G genotype with a decreased risk for RF-positive rheumatoid arthritis.

82. (previously presented) The method of claim 56, further comprising correlating the presence of said T allele or said A allele with an increased risk for RF-positive rheumatoid arthritis,

or correlating the presence of said homozygous C/C genotype or said homozygous G/G genotype with a decreased risk for RF-positive rheumatoid arthritis.

83. (previously presented) The method of any one of claims 80, 81, and 82, wherein said correlating is performed by computer software.

84. (previously presented) The method of any one of claims 36, 46, and 56 which is an automated method.

85. (previously presented) The method of claim 67, wherein the report is in paper form or computer readable medium form.

86. (previously presented) The method of claim 68, wherein the report is in paper form or computer readable medium form.

87. (previously presented) The method of claim 69, wherein the report is in paper form or computer readable medium form.

88. (previously presented) The method of claim 70, wherein the report is in paper form or computer readable medium form.

89. (previously presented) The method of claim 71, wherein the report is in paper form or computer readable medium form.

90. (previously presented) The method of claim 72, wherein the report is in paper form or computer readable medium form.

91. (new) The method of claim 46, wherein said testing is performed using an allele-specific method.

92. (new) The method of claim 91, wherein said allele-specific method is allele-specific probe hybridization, allele-specific primer extension, or allele-specific amplification.

93. (new) The method of claim 91, wherein said allele-specific method detects a C allele of said C/C genotype or a G allele of said G/G genotype.

94. (new) A method of determining whether a human has an increased risk for RF-positive rheumatoid arthritis, comprising:

a) testing nucleic acid from said human for the presence or absence of at least one T allele at a polymorphism in gene *PTPN22* at position 101 of SEQ ID NO:36673 or at least one A allele at position 101 of its complement; and

b) correlating the presence of said T allele or said A allele with said human having said increased risk for RF-positive rheumatoid arthritis, or the absence of said T allele or said A allele with said human having no said increased risk for RF-positive rheumatoid arthritis.

95. (new) The method of claim 94, wherein said correlating is performed by computer software.

96. (new) The method of claim 94, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human.

97. (new) The method of claim 96, wherein said biological sample is blood, saliva, or buccal cells.

98. (new) The method of claim 96, further comprising preparing said nucleic acid extract from said biological sample prior to said testing.

99. (new) The method of claim 98, further comprising obtaining said biological sample from said human prior to said preparing.

100. (new) The method of claim 94, wherein said testing comprises nucleic acid amplification.

101. (new) The method of claim 100, wherein said nucleic acid amplification is carried out by polymerase chain reaction.

102. (new) The method of any one of claims 94 to 101, wherein said testing is performed using sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, single-stranded conformation polymorphism analysis, or denaturing gradient gel electrophoresis (DGGE).

103. (new) The method of any one of claims 94 to 101, wherein said testing is performed using an allele-specific method.

104. (new) The method of claim 103, wherein said allele-specific method is allele-specific probe hybridization, allele-specific primer extension, or allele-specific amplification.

105. (new) The method of claim 103, wherein said allele-specific method detects said T allele or said A allele.

106. (new) The method of claim 94 which is an automated method.

107. (new) The method of any one of claims 36, 56, and 94 wherein said human is homozygous for said T allele or said A allele.

108. (new) The method of any one of claims 36, 56, and 94 wherein said human is heterozygous for said T allele or said A allele.